

## SEQUENCE LISTING

<110> Gross, Jane A.  
 Xu, Wenfeng  
 Madden, Karen  
 Yee, David P.

<120> SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING

<130> 98-75C2

<150> 60/115,068

<151> 1999-01-07

<150> 60/169,890

<151> 1999-12-09

<150> 09/479,856

<151> 2000-01-07

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<151> 2000-05-11

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| gagta | atg | agt | ggc | ctg | ggc | cgg | agc | agg | cga | ggt | ggc | cgg | agc | cgt | gtg | 50 |
|       | Met | Ser | Gly | Leu | Gly | Arg | Ser | Arg | Arg | Gly | Gly | Arg | Ser | Arg | Val |    |
|       | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| gac | cag | gag | gag | cgc | tgg | tca | ctc | agc | tgc | cgc | aag | gag | caa | ggc | aag | 98 |
| Asp | Gln | Glu | Glu | Arg | Trp | Ser | Leu | Ser | Cys | Arg | Lys | Glu | Gln | Gly | Lys |    |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |    |

00220"9022960

|   |     |
|---|-----|
| ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt | 146 |
| Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys |     |
| 35 40 45  |     |
| gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg | 194 |
| Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg |     |
| 50 55 60  |     |
| agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa | 242 |
| Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu |     |
| 65 70 75  |     |
| gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag cac | 290 |
| Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His |     |
| 80 85 90 95   |     |
| aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca | 338 |
| Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala |     |
| 100 105 110   |     |
| gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt gcc | 386 |
| Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala |     |
| 115 120 125   |     |
| gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag agg | 434 |
| Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg |     |
| 130 135 140   |     |
| ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt ccg | 482 |
| Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro |     |
| 145 150 155   |     |
| gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg agc | 530 |
| Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser |     |
| 160 165 170 175   |     |
| aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag tgc | 578 |
| Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys |     |
| 180 185 190   |     |
| agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac ccc | 626 |
| Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro |     |
| 195 200 205   |     |
| act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg cag | 674 |

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Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln  
 210 215 220

cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg cct 722  
 Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro  
 225 230 235

gcc cag gag ggg ggc cca ggt gca taaatggggg tcaggaggagg aaaggaggag 776  
 Ala Gln Glu Gly Gly Pro Gly Ala  
 240 245

ggagagagat ggagaggagg ggagagagaa agagaggtgg ggagagggga gagagatatg 836  
 aggagagaga gacagaggag gcagagaggg agagaaacag aggagacaga gagggagaga 896  
 gagacagagg gagagagaga cagaggggaa gagaggcaga gagggaaaga ggcagagaag 956  
 gaaagaggca gagagggaga gaggcagaga gggagagagg cagagagaca gagagggaga 1016  
 gagggacaga gagagataga gcaggaggtc ggggcactct gagtcccagt tccagtgca 1076  
 gctgtaggtc gtcacacacct aaccacacgt gcaataaagt cctcgtgcct gctgctcaca 1136  
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 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly  
 35 40 45  
 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser  
 50 55 60  
 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val  
 65 70 75 80  
 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg  
 85 90 95  
 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp  
 100 105 110  
 Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val  
 115 120 125  
 Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly  
 130 135 140  
 Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala  
 145 150 155 160

00220"0022000

Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr  
                           165                          170                          175  
 Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg  
                           180                          185                          190  
 Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr  
                           195                          200                          205  
 Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro  
                           210                          215                          220  
 Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala  
 225                          230                          235                          240  
 Gln Glu Gly Gly Pro Gly Ala  
                           245

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cag gag gag cgc tgg tca ctc agc tgc cgc aag gag caa ggc aag ttc 96  
 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe  
                           20                          25                          30

tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt gga 144  
 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly  
                           35                          40                          45

cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg agc 192  
 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser  
                           50                          55                          60

cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa gtt 240  
 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val  
   65                          70                          75                          80

gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag cac aga 288  
 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg

002220"9022200

85

90

95

ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca gat 336  
 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp  
           100                          105                          110

cag gtg gcc ctg gtc tac agc acg 360  
 Gln Val Ala Leu Val Tyr Ser Thr  
           115                          120

&lt;210&gt; 4

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp  
 1                          5                          10                          15  
 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe  
           20                          25                          30  
 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly  
           35                          40                          45  
 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser  
           50                          55                          60  
 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val  
 65                          70                          75                          80  
 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg  
           85                          90                          95  
 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp  
           100                          105                          110  
 Gln Val Ala Leu Val Tyr Ser Thr  
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&lt;211&gt; 1377

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; (14)...(895)

&lt;400&gt; 5

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| Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     |     |     |
| agc   | cgt | gtg | gac | cag | gag | gag | cgc | ttt | cca | cag | ggc | ctg | tgg | acg | ggg |
| Ser   | Arg | Val | Asp | Gln | Glu | Glu | Arg | Phe | Pro | Gln | Gly | Leu | Trp | Thr | Gly |
| 15  |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     |     |     |
| gtg   | gct | atg | aga | tcc | tgc | ccc | gaa | gag | cag | tac | tgg | gat | cct | ctg | ctg |
| Val   | Ala | Met | Arg | Ser | Cys | Pro | Glu | Glu | Gln | Tyr | Trp | Asp | Pro | Leu | Leu |
| 30  |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     |     |     |
| ggt   | acc | tgc | atg | tcc | tgc | aaa | acc | att | tgc | aac | cat | cag | agc | cag | cgc |
| Gly   | Thr | Cys | Met | Ser | Cys | Lys | Thr | Ile | Cys | Asn | His | Gln | Ser | Gln | Arg |
| 45  |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| acc   | tgt | gca | gcc | ttc | tgc | agg | tca | ctc | agc | tgc | cgc | aag | gag | caa | ggc |
| Thr   | Cys | Ala | Ala | Phe | Cys | Arg | Ser | Leu | Ser | Cys | Arg | Lys | Glu | Gln | Gly |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     |     |
| aag   | ttc | tat | gac | cat | ctc | ctg | agg | gac | tgc | atc | agc | tgt | gcc | tcc | atc |
| Lys   | Phe | Tyr | Asp | His | Leu | Leu | Arg | Asp | Cys | Ile | Ser | Cys | Ala | Ser | Ile |
| 80  |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     |     |
| tgt   | gga | cag | cac | cct | aag | caa | tgt | gca | tac | ttc | tgt | gag | aac | aag | ctc |
| Cys   | Gly | Gln | His | Pro | Lys | Gln | Cys | Ala | Tyr | Phe | Cys | Glu | Asn | Lys | Leu |
| 95  |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     |     |     |
| agg   | agc | cca | gtg | aac | ctt | cca | cca | gag | ctc | agg | aga | cag | cgg | agt | gga |
| Arg   | Ser | Pro | Val | Asn | Leu | Pro | Pro | Glu | Leu | Arg | Arg | Gln | Arg | Ser | Gly |
| 110   |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |
| gaa   | gtt | gaa | aac | aat | tca | gac | aac | tcg | gga | agg | tac | caa | gga | ttg | gag |
| Glu   | Val | Glu | Asn | Asn | Ser | Asp | Asn | Ser | Gly | Arg | Tyr | Gln | Gly | Leu | Glu |
| 125   |     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |
| cac   | aga | ggc | tca | gaa | gca | agt | cca | gct | ctc | ccg | ggg | ctg | aag | ctg | agt |
| His   | Arg | Gly | Ser | Glu | Ala | Ser | Pro | Ala | Leu | Pro | Gly | Leu | Lys | Leu | Ser |
| 145   |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     |     |     |
| gca   | gat | cag | gtg | gcc | ctg | gtc | tac | agc | acg | ctg | ggg | ctc | tgc | ctg | tgt |
| Ala   | Asp | Gln | Val | Ala | Leu | Val | Tyr | Ser | Thr | Leu | Gly | Leu | Cys | Leu | Cys |
| 160   |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     |     |     |
| gcc   | gtc | ctc | tgc | tgc | ttc | ctg | gtg | gcg | gtg | gcc | tgc | ttc | ctc | aag | aag |
| Ala   | Val | Leu | Cys | Cys | Phe | Leu | Val | Ala | Val | Ala | Cys | Phe | Leu | Lys | Lys |

002220 " 90223950

| 175  | 180 | 185 |      |
|--|-----|-----|------|
| agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt    |     |     | 625  |
| Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser    |     |     |      |
| 190  | 195 | 200 |      |
| ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg    |     |     | 673  |
| Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val    |     |     |      |
| 205  | 210 | 215 | 220  |
| agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag    |     |     | 721  |
| Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu    |     |     |      |
|  | 225 | 230 | 235  |
| tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac    |     |     | 769  |
| Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp    |     |     |      |
|  | 240 | 245 | 250  |
| ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg    |     |     | 817  |
| Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu    |     |     |      |
|  | 255 | 260 | 265  |
| cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg    |     |     | 865  |
| Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val    |     |     |      |
|  | 270 | 275 | 280  |
| cct gcc cag gag ggg ggc cca ggt gca taa atgggggtca gggagggaaa      |     |     | 915  |
| Pro Ala Gln Glu Gly Gly Pro Gly Ala *                              |     |     |      |
| 285  | 290 |     |      |
| ggaggagggga gagagatgga gaggagggga gagagaaaga gaggtgggga gaggggagag |     |     | 975  |
| agatatgagg agagagagac agaggaggca gaaagggaga gaaacagagg agacagagag  |     |     | 1035 |
| ggagagagag acagagggag agagagacag aggggaagag aggcagagag ggaaagaggc  |     |     | 1095 |
| agagaaggaa agagacaggc agagaaggag agaggcagag agggagagag gcagagaggg  |     |     | 1155 |
| agagaggcag agagacagag agggagagag ggacagagag agatagagca ggaggtcggg  |     |     | 1215 |
| gcactctgag tcccagttcc cagtgcagct gtaggtcgtc atcacctaac cacacgtgca  |     |     | 1275 |
| ataaagtcc cgtgcctgct gctcacagcc cccgagagcc cctcctcctg gagaataaaa   |     |     | 1335 |
| cctttggcag ctgcccttcc tcaaaaaaaaa aaaaaaaaaa aa                    |     |     | 1377 |

&lt;210&gt; 6

&lt;211&gt; 293

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

09627206 "072700

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gly | Leu | Gly | Arg | Ser | Arg | Arg | Gly | Gly | Arg | Ser | Arg | Val | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Glu | Glu | Arg | Phe | Pro | Gln | Gly | Leu | Trp | Thr | Gly | Val | Ala | Met | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Cys | Pro | Glu | Glu | Gln | Tyr | Trp | Asp | Pro | Leu | Leu | Gly | Thr | Cys | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Cys | Lys | Thr | Ile | Cys | Asn | His | Gln | Ser | Gln | Arg | Thr | Cys | Ala | Ala |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Cys | Arg | Ser | Leu | Ser | Cys | Arg | Lys | Glu | Gln | Gly | Lys | Phe | Tyr | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| His | Leu | Leu | Arg | Asp | Cys | Ile | Ser | Cys | Ala | Ser | Ile | Cys | Gly | Gln | His |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Lys | Gln | Cys | Ala | Tyr | Phe | Cys | Glu | Asn | Lys | Leu | Arg | Ser | Pro | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Leu | Pro | Pro | Glu | Leu | Arg | Arg | Gln | Arg | Ser | Gly | Glu | Val | Glu | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Ser | Asp | Asn | Ser | Gly | Arg | Tyr | Gln | Gly | Leu | Glu | His | Arg | Gly | Ser |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Glu | Ala | Ser | Pro | Ala | Leu | Pro | Gly | Leu | Lys | Leu | Ser | Ala | Asp | Gln | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Leu | Val | Tyr | Ser | Thr | Leu | Gly | Leu | Cys | Leu | Cys | Ala | Val | Leu | Cys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Cys | Phe | Leu | Val | Ala | Val | Ala | Cys | Phe | Leu | Lys | Lys | Arg | Gly | Asp | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Cys | Ser | Cys | Gln | Pro | Arg | Ser | Arg | Pro | Arg | Gln | Ser | Pro | Ala | Lys | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Gln | Asp | His | Ala | Met | Glu | Ala | Gly | Ser | Pro | Val | Ser | Thr | Ser | Pro |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Pro | Val | Glu | Thr | Cys | Ser | Phe | Cys | Phe | Pro | Glu | Cys | Arg | Ala | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

09627206 "072700



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<212> DNA
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Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser Leu Leu His Ala Cys Ile  
10 15 20

cct tgt caa ctt cga tgt tct tct aat act cct cct cta aca tgt cag 332  
Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln  
25 30 35

cgt tat tgt aat gca agt gtg acc aat tca gtg aaa gga acg aat gcg 380  
Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Thr Asn Ala  
40 45 50

att ctc tgg acc tgt ttg gga ctg agc tta ata att tct ttg gca gtt 428  
Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu Ile Ile Ser Leu Ala Val  
55 60 65 70

ttc gtg cta atg ttt ttg cta agg aag ata agc tct gaa cca tta aag 476  
 Phe Val Leu Met Phe Leu Leu Arg Lys Ile Ser Ser Glu Pro Leu Lys  
                     75                    80                    85

gac gag ttt aaa aac aca gga tca ggt ctc ctg ggc atg gct aac att 524  
 Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu Leu Gly Met Ala Asn Ile  
                     90                    95                    100

gac ctg gaa aag agc agg act ggt gat gaa att att ctt ccg aga ggc 572  
 Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu Ile Ile Leu Pro Arg Gly  
                     105                    110                    115

ctc gag tac acg gtg gaa gaa tgc acc tgt gaa gac tgc atc aag agc 620  
 Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys Glu Asp Cys Ile Lys Ser  
                     120                    125                    130

aaa ccg aag gtc gac tct gac cat tgc ttt cca ctc cca gct atg gag 668  
 Lys Pro Lys Val Asp Ser Asp His Cys Phe Pro Leu Pro Ala Met Glu  
                     135                    140                    145                    150

gaa ggc gca acc att ctt gtc acc acg aaa acg aat gac tat tgc aag 716  
 Glu Gly Ala Thr Ile Leu Val Thr Thr Lys Thr Asn Asp Tyr Cys Lys  
                     155                    160                    165

agc ctg cca gct gct ttg agt gct acg gag ata gag aaa tca att tct 764  
 Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu Ile Glu Lys Ser Ile Ser  
                     170                    175                    180

gct agg taa ttaaccattt cgactcgagc agtgccactt taaaaatctt 813  
 Ala Arg \*

ttgtcagaat agatgatgtg tcagatctct ttaggatgac tgtatttttc agttgccgat 873  
 acagcttttt gtcctctaac tgtggaaact ctttatgtta gatataattc tctaggttac 933  
 tgttggggagc ttaatggtag aaacttcctt ggtttcatga ttaaagtctt tttttttcct 993  
 ga 995

<210> 8

<211> 184

<212> PRT

<213> Homo sapiens

<400> 8

Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser  
   1                    5                    10                    15

Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr  
                   20                  25                  30  
 Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser  
           35                  40                  45  
 Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu  
       50                  55                  60  
 Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile  
 65                  70                  75                  80  
 Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu  
                   85                  90                  95  
 Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu  
           100                  105                  110  
 Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys  
       115                  120                  125  
 Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe  
       130                  135                  140  
 Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys  
 145                  150                  155                  160  
 Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu  
                   165                  170                  175  
 Ile Glu Lys Ser Ile Ser Ala Arg  
           180

&lt;210&gt; 9

&lt;211&gt; 245

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp Gln Glu Glu Arg  
 1                  5                  10                  15  
 Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg Ser Cys Pro Glu  
           20                  25                  30  
 Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys Lys Thr  
       35                  40                  45  
 Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser  
       50                  55                  60  
 Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg  
 65                  70                  75                  80  
 Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys  
                   85                  90                  95  
 Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val Asn Leu Pro Pro  
           100                  105                  110  
 Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn Asn Ser Asp Asn  
       115                  120                  125

002220"90222960

Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser Glu Ala Ser Pro  
 130 135 140  
 Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val Ala Leu Val Tyr  
 145 150 155 160  
 Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys Cys Phe Leu Val  
 165 170 175  
 Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro Cys Ser Cys Gln  
 180 185 190  
 Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser Ser Gln Asp His  
 195 200 205  
 Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro Glu Pro Val Glu  
 210 215 220  
 Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro Thr Gln Glu Ser  
 225 230 235 240  
 Ala Val Thr Pro Gly  
 245

<210> 10

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Motif describing the cysteine-rich pseudo-repeat domain

<221> VARIANT

<222> (1)...(2)

<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<221> VARIANT

<222> (4)...(4)

<223> Xaa is any amino acid residue except cysteine.

<221> VARIANT

<222> (5)...(5)

<223> Xaa is glutamine, glutamic acid, or lysine.

<221> VARIANT

<222> (6)...(6)

<223> Xaa is glutamine, glutamic acid, lysine, asparagine, arginine, aspartic acid, histidine, or serine.

<223> Xaa is glutamine or glutamic acid.

<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<223> Xaa is tyrosine, phenylalanine, or tryptophan.

<223> Xaa is any amino acid residue except cysteine.

<223> Each Xaa is independently any amino acid residue except cysteine.

<223> Xaa is isoleucine, methionine, leucine, or valine.

<223> Xaa is any amino acid residue except cysteine.

<223> Each Xaa is independently any amino acid residue except cysteine.

<223> Each Xaa is independently any amino acid residue except cysteine.

<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<221> VARIANT

<222> (35)...(36)

<223> Each Xaa is independently any amino acid residue except cysteine.

<221> VARIANT

<222> (37)...(37)

<223> Xaa is tyrosine or phenylalanine.

<221> VARIANT

<222> (39)...(40)

<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<400> 10

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Cys | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Asp | Xaa | Leu | Leu | Xaa |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| Xaa | Cys | Xaa | Xaa | Cys | Xaa | Xaa | Xaa | Cys | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Xaa | Cys | Xaa | Xaa | Xaa | Cys | Xaa | Xaa |     |     |     |     |     |     |     |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     |     |     |     |     |

<210> 11

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide sequence encoding the polypeptide of SEQ ID NO:4

<221> variation

<222> (1)...(360)

<223> Each N is independently A, T, G, or C.

<400> 11

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgwsnggny | tnggmgnws  | nmgnmgnggn | ggmgnwsnm  | ngtngayca  | rgargarmgn | 60  |
| tggsnytnw  | sntgymgnaa | rgarcarggn | aarttytayg | aycayytnyt | nmngaytg   | 120 |
| athwsntgyg | cnwsnathtg | yggncarcay | ccnaarcart | gygcntaytt | ytgygaraay | 180 |
| aarytnmgw  | snccngtnaa | yytnccncn  | garytnmgm  | gncarmgnws | ngngargtn  | 240 |
| garaayaayw | sngayaayws | ngnmngntay | carggnytn  | arcaymgngg | nwsngargcn | 300 |
| wsnccngcny | tnccnggnyt | naarytnwsn | gcngaycarg | tngcnytngt | ntaywsnacb | 360 |

<210> 12

<211> 741  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Degenerate oligonucleotide sequence encoding a polypeptide of SEQ ID NO:2

<221> variation  
 <222> (1)...(741)  
 <223> Each N is independently A, T, G, or C.

<400> 12

|   |     |
|---|-----|
| atgwsnggny tnggmgrnws nmgnmgnggn ggnmgwnsm gngtngayca rgargarmgn  | 60  |
| tggwsnytnw sntgymgnaa rgarcarggn aarttytayg aycayytnyt nmngaytgy  | 120 |
| athwsntgyg cnwsnathtg yggncarcay ccnaarcart gygcntaytt ytgygaraay | 180 |
| aarytnmgmw snccngtnaa yytnccnccn garytnmgm gncarmgnws ngngargtn   | 240 |
| garaayaayw sngayaayws nggnmgntay carggnytn gncaymgngg nwsngargcn  | 300 |
| wsnccngcny tnccnggnyt naarytnwsn gcngaycarg tngcnytngt ntaywsnacn | 360 |
| ytnggnytn gyytnygygc ngtnytnygy tgyttyytn tngcngtngc ntgyttyytn   | 420 |
| aaraarmgng gngayccntg ywsntgyar ccnmgnwnsm gncnmgna rwsnccngcn    | 480 |
| aarwsnwsnc argaycaygc natggargcn ggnwsnccng tnwsnacnws nccngarccn | 540 |
| gtngaracnt gywsnttytg yttccngar tgymgngcnc cnacncarga rwsngcngtn  | 600 |
| acnccnggna cncngaycc nacntgygc gnmngntgg gntgycayac nmgnacnacn    | 660 |
| gtnytnarc cntgyccnca yathccngay wsnggnytn gnathgtntg ygtncngcn    | 720 |
| cargargng gncngngc n  | 741 |

<210> 13  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> FLAG tag

<400> 13  
 Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

<210> 14  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>

0067206-072700

<223> Glu-Glu tag

<400> 14

Glu Glu Tyr Met Pro Met Glu

1

5

<210> 15

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC19980

<400> 15

cgaagagcag tactgggatc ctct

24

<210> 16

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC19981

<400> 16

gccaaaggcca ctgtctggga tgt

23

<210> 17

<211> 1149

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (236)...(1027)

<400> 17

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gaattcggca | cgaggcagaa | aggagaaaat | tcaggataac | tctcctgagg | ggtgagccaa | 60  |
| gccctgccat | gtagtgcacg | caggacatca | acaaacacag | ataacaggaa | atgatccatt | 120 |
| ccctgtggtc | acttattcta | aaggccccaa | ccttcaaagt | tcaagtagtg | atatggatga | 180 |
| ctccacagaa | agggagcagt | cacgccttac | ttcttgccct | aagaaaagag | aagaa atg  | 238 |
|            |            |            |            |            | Met        |     |
|            |            |            |            |            | 1          |     |

002220"90222960



|   |     |
|---|-----|
| aaa ctg aag gag tgt gtt tcc atc ctc cca cgg aag gaa agc ccc tct | 286 |
| Lys Leu Lys Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser |     |
| 5 10 15   |     |
| gtc cga tcc tcc aaa gac gga aag ctg ctg gct gca acc ttg ctg ctg | 334 |
| Val Arg Ser Ser Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Leu |     |
| 20 25 30  |     |
| gca ctg ctg tct tgc tgc ctc acg gtg gtg tct ttc tac cag gtg gcc | 382 |
| Ala Leu Leu Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala |     |
| 35 40 45  |     |
| gcc ctg caa ggg gac ctg gcc agc ctc cgg gca gag ctg cag ggc cac | 430 |
| Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His |     |
| 50 55 60 65   |     |
| cac gcg gag aag ctg cca gca gga gca gga gcc ccc aag gcc ggc ctg | 478 |
| His Ala Glu Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu |     |
| 70 75 80  |     |
| gag gaa gct cca gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca | 526 |
| Glu Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro Pro |     |
| 85 90 95  |     |
| gct cca gga gaa ggc aac tcc agt cag aac agc aga aat aag cgt gcc | 574 |
| Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg Ala |     |
| 100 105 110   |     |

004270"90272960

gtt cag ggt cca gaa gaa aca gtc act caa gac tgc ttg caa ctg att 622  
Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu Ile  
115 120 125

gca gac agt gaa aca cca act ata caa aaa gga tct tac aca ttt gtt 670  
Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe Val  
130 135 140 145

cca tgg ctt ctc agc ttt aaa agg gga agt gcc cta gaa gaa aaa gag 718  
Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu  
150 155 160

aat aaa ata ttg gtc aaa gaa act ggt tac ttt ttt ata tat ggt cag 766  
Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr Gly Gln  
165 170 175

gtt tta tat act gat aag acc tac gcc atg gga cat cta att cag agg 814  
Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln Arg  
180 185 190

aag aag gtc cat gtc ttt ggg gat gaa ttg agt ctg gtg act ttg ttt 862  
Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe  
195 200 205

cga tgt att caa aat atg cct gaa aca cta ccc aat aat tcc tgc tat 910  
Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys Tyr  
210 215 220 225

tca gct ggc att gca aaa ctg gaa gaa gga gat gaa ctc caa ctt gca 958  
Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu Ala  
230 235 240

ata cca aga gaa aat gca caa ata tca ctg gat gga gat gtc aca ttt 1006  
Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr Phe  
245 250 255

ttt ggt gca ttg aaa ctg ctg tgacctactt acaccatgtc tgtagctatt 1057  
Phe Gly Ala Leu Lys Leu Leu  
260

ttcctccctt tctctgtacc tctaagaaga aagaatctaa ctgaaaatac caaaaaaaaa 1117  
aaaaaaaaaa aaaaaaccct cgagcggccg cc 1149

&lt;210&gt; 18

&lt;211&gt; 264

09627206.072700

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro  
 1 5 10 15  
 Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu  
 20 25 30  
 Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val  
 35 40 45  
 Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly  
 50 55 60  
 His His Ala Glu Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly  
 65 70 75 80  
 Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro  
 85 90 95  
 Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg  
 100 105 110  
 Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu  
 115 120 125  
 Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe  
 130 135 140  
 Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys  
 145 150 155 160  
 Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr Gly  
 165 170 175  
 Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln  
 180 185 190  
 Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu  
 195 200 205  
 Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys  
 210 215 220  
 Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu  
 225 230 235 240  
 Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr  
 245 250 255  
 Phe Phe Gly Ala Leu Lys Leu Leu  
 260

&lt;210&gt; 19

&lt;211&gt; 1430

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

0042206 "072700

&lt;221&gt; CDS

&lt;222&gt; (102)...(848)

&lt;400&gt; 19

|  |                     |
|--|---------------------|
| ttggcgcagg agcgtgcgta ggattgctcg ctcacaacag gcacctgact ggtattgaaa  | 60                  |
| gccgagtcctt cccttcctct ttaaaggatt ggtgaccagg c atg gct atg gca ttc | 116                 |
|  | Met Ala Met Ala Phe |
|  | 1 5                 |

|   |          |
|---|----------|
| tgc ccc aaa gat cag tac tgg gac tcc tca agg aaa tcc tgt gtc tcc | 164      |
| Cys Pro Lys Asp Gln Tyr Trp Asp Ser Ser Arg Lys Ser Cys Val Ser |          |
|   | 10 15 20 |

|   |          |
|---|----------|
| tgt gca ctg acc tgc agc cag agg agc cag cgc acc tgt aca gac ttc | 212      |
| Cys Ala Leu Thr Cys Ser Gln Arg Ser Gln Arg Thr Cys Thr Asp Phe |          |
|   | 25 30 35 |

|   |          |
|---|----------|
| tgc aaa ttc atc aat tgc cga aaa gag caa ggc agg tac tac gac cat | 260      |
| Cys Lys Phe Ile Asn Cys Arg Lys Glu Gln Gly Arg Tyr Tyr Asp His |          |
|   | 40 45 50 |

|   |          |
|---|----------|
| ctc ctg ggg gcc tgc gtc agc tgt gac tcc acc tgc aca cag cac cct | 308      |
| Leu Leu Gly Ala Cys Val Ser Cys Asp Ser Thr Cys Thr Gln His Pro |          |
|   | 55 60 65 |

|   |             |
|---|-------------|
| cag cag tgt gcc cac ttc tgt gag aaa agg ccc aga agc cag gcg aac | 356         |
| Gln Gln Cys Ala His Phe Cys Glu Lys Arg Pro Arg Ser Gln Ala Asn |             |
|   | 70 75 80 85 |

|   |           |
|---|-----------|
| ctc cag ccc gag ctc ggg aga cca cag gcc ggg gag gtg gaa gtc agg | 404       |
| Leu Gln Pro Glu Leu Gly Arg Pro Gln Ala Gly Glu Val Glu Val Arg |           |
|   | 90 95 100 |

|   |             |
|---|-------------|
| tca gac aac tca gga agg cac cag gga tct gag cat ggt cca gga ttg | 452         |
| Ser Asp Asn Ser Gly Arg His Gln Gly Ser Glu His Gly Pro Gly Leu |             |
|   | 105 110 115 |

002270" 9022950

agg cta agt agc gac cag ctg act ctc tac tgc aca ctg ggg gtc tgc 500  
 Arg Leu Ser Ser Asp Gln Leu Thr Leu Tyr Cys Thr Leu Gly Val Cys  
           120                                  125                                  130

ctc tgc gcc atc ttc tgc tgt ttc ttg gtg gcc ttg gcc tcc ttc ctc 548  
 Leu Cys Ala Ile Phe Cys Cys Phe Leu Val Ala Leu Ala Ser Phe Leu  
           135                                  140                                  145

agg cgt aga gga gag cca cta ccc agc cag cct gcc ggg cca cgt ggg 596  
 Arg Arg Arg Gly Glu Pro Leu Pro Ser Gln Pro Ala Gly Pro Arg Gly  
 150                                  155                                  160                                  165

tca caa gca aac tct ccc cac gcc cac cgc ccc gtg aca gag gct tgc 644  
 Ser Gln Ala Asn Ser Pro His Ala His Arg Pro Val Thr Glu Ala Cys  
                                   170                                  175                                  180

gac gag gtg acc gcg tca ccc cag cct gtg gaa acg tgt agc ttc tgc 692  
 Asp Glu Val Thr Ala Ser Pro Gln Pro Val Glu Thr Cys Ser Phe Cys  
                                   185                                  190                                  195

ttc ccg gag cgc agt tct ccc act cag gag agc gcg ccg cgt tcg ctc 740  
 Phe Pro Glu Arg Ser Ser Pro Thr Gln Glu Ser Ala Pro Arg Ser Leu  
                                   200                                  205                                  210

ggg ata cac ggc ttc gcg ggc act gcc gcc ccg cag ccc tgt atg cgt 788  
 Gly Ile His Gly Phe Ala Gly Thr Ala Ala Pro Gln Pro Cys Met Arg  
           215                                  220                                  225

gca aca gta ggc ggc ctg ggt gtc ctg cgc gca tcc act ggg gac gct 836  
 Ala Thr Val Gly Gly Leu Gly Val Leu Arg Ala Ser Thr Gly Asp Ala  
 230                                  235                                  240                                  245

cgt ccg gca act tgacagcccg aaaaataaaa aagacaattt agaggatgga 888  
 Arg Pro Ala Thr

gtgacagagg gggaaagga tggagaagag acagatgaag acacgataaa ggaagcccgg 948  
 ctgcacccac gcagagcaac aaagcaacca cctgcagcgc ccacgttccc agcaccgcct 1008  
 gtgcctgccg ctgtgtccta tactttccag agcagtcaac ctgtgccttt tttctttagt 1068  
 cgagaaagat ggagaatgac cggcacctag cattaccctt acaattctta caaacaagtg 1128  
 gtctttccta tggccttagg cagatagctg agtgcagtgt ggatgtattt gtgatttaag 1188  
 taacttgtat gtgtatgtgc agattcgggg ttatgtcata tgtgcatgta tacgtgagtt 1248  
 gtgtgtctgt atgagttgtg tgtatatgtg cgcctataaa tatgtgtgtg aattctgtgc 1308  
 atgcagatgt gtgtgtacat atgtgtctgg ctgatgtggt atagccagaa agatgagggc 1368  
 ccttctaggt gaaggccaaa catctaaaaa ccatctaggt gatgggtgct cgtgccgaat 1428

tc

1430

<210> 20  
 <211> 249  
 <212> PRT  
 <213> Mus musculus

<400> 20

Met Ala Met Ala Phe Cys Pro Lys Asp Gln Tyr Trp Asp Ser Ser Arg  
 1 5 10 15  
 Lys Ser Cys Val Ser Cys Ala Leu Thr Cys Ser Gln Arg Ser Gln Arg  
 20 25 30  
 Thr Cys Thr Asp Phe Cys Lys Phe Ile Asn Cys Arg Lys Glu Gln Gly  
 35 40 45  
 Arg Tyr Tyr Asp His Leu Leu Gly Ala Cys Val Ser Cys Asp Ser Thr  
 50 55 60  
 Cys Thr Gln His Pro Gln Gln Cys Ala His Phe Cys Glu Lys Arg Pro  
 65 70 75 80  
 Arg Ser Gln Ala Asn Leu Gln Pro Glu Leu Gly Arg Pro Gln Ala Gly  
 85 90 95  
 Glu Val Glu Val Arg Ser Asp Asn Ser Gly Arg His Gln Gly Ser Glu  
 100 105 110  
 His Gly Pro Gly Leu Arg Leu Ser Ser Asp Gln Leu Thr Leu Tyr Cys  
 115 120 125  
 Thr Leu Gly Val Cys Leu Cys Ala Ile Phe Cys Cys Phe Leu Val Ala  
 130 135 140  
 Leu Ala Ser Phe Leu Arg Arg Arg Gly Glu Pro Leu Pro Ser Gln Pro  
 145 150 155 160  
 Ala Gly Pro Arg Gly Ser Gln Ala Asn Ser Pro His Ala His Arg Pro  
 165 170 175  
 Val Thr Glu Ala Cys Asp Glu Val Thr Ala Ser Pro Gln Pro Val Glu  
 180 185 190  
 Thr Cys Ser Phe Cys Phe Pro Glu Arg Ser Ser Pro Thr Gln Glu Ser  
 195 200 205  
 Ala Pro Arg Ser Leu Gly Ile His Gly Phe Ala Gly Thr Ala Ala Pro  
 210 215 220  
 Gln Pro Cys Met Arg Ala Thr Val Gly Gly Leu Gly Val Leu Arg Ala  
 225 230 235 240  
 Ser Thr Gly Asp Ala Arg Pro Ala Thr  
 245

<210> 21  
 <211> 473  
 <212> DNA  
 <213> Artificial Sequence

002220"90272960

&lt;220&gt;

&lt;223&gt; Northern Blot Probe

&lt;400&gt; 21

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| ctgtggacgg | gggtggctat | gagatcctgc | cccgaagagc | agtactggga | tcctctgctg  | 60  |
| ggtacctgca | tgtcctgcaa | aaccatttgc | aaccatcaga | gccagcgcac | ctgtgcagcc  | 120 |
| ttctgcaggt | cactcagctg | ccgcaaggag | caaggcaagt | tctatgacca | tctcctgagg  | 180 |
| gactgcatca | gctgtgcctc | catctgtgga | cagcacccta | agcaatgtgc | atacttctgt  | 240 |
| gagaacaagc | tcaggagccc | agtgaacctt | ccaccagagc | tcaggagaca | gcggagtgga  | 300 |
| gaagttgaaa | acaattcaga | caactcggga | aggtaccaag | gattggagca | cagaggctca  | 360 |
| gaagcaagtc | cagctctccc | ggggctgaag | ctgagtgcag | atcaggtggc | cctgggtctac | 420 |
| agcacgctgg | ggctctgcct | gtgtgccgtc | ctctgctgct | tcctggtggc | ggt         | 473 |

&lt;210&gt; 22

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; ZC20061

&lt;400&gt; 22

|            |            |       |    |
|------------|------------|-------|----|
| ctgtggacag | gggtggctat | gagat | 25 |
|------------|------------|-------|----|

&lt;210&gt; 23

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide ZC20062

&lt;400&gt; 23

|            |            |       |    |
|------------|------------|-------|----|
| accgccacca | ggaagcacag | aggac | 25 |
|------------|------------|-------|----|

&lt;210&gt; 24

&lt;211&gt; 256

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Northern Blot probe

&lt;400&gt; 24

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|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tgcgattctc | tggacctgtt | tgggactgag | cttaataatt | tctttggcag | ttttcgtgct | 60  |
| aatgtttttg | ctaaggaaga | taagctctga | accattaaag | gacgagttta | aaaacacagg | 120 |
| atcaggtctc | ctgggcatgg | ctaacattga | cctggaaaag | agcaggactg | gtgatgaaat | 180 |
| tattcttccg | agaggcctcg | agtacacggt | ggaagaatgc | acctgtgaag | actgcatcaa | 240 |
| gagcaaaccg | aaggtc     |            |            |            |            | 256 |

&lt;210&gt; 25

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide ZC21065

&lt;400&gt; 25

|            |            |    |    |
|------------|------------|----|----|
| tgcgattctc | tggacctgtt | tg | 22 |
|------------|------------|----|----|

&lt;210&gt; 26

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide ZC21067

&lt;400&gt; 26

|            |            |    |    |
|------------|------------|----|----|
| gaccttcggt | ttgctcttga | tg | 22 |
|------------|------------|----|----|

&lt;210&gt; 27

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide ZC24200

&lt;400&gt; 27

|            |            |    |
|------------|------------|----|
| acactggggg | tctgcctctg | 20 |
|------------|------------|----|

&lt;210&gt; 28

&lt;211&gt; 17

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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<223> Oligonucleotide ZC24201

<400> 28

gcgaagccgt gtatccc

17

<210> 29

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC24198

<400> 29

tctacagcac gctgggg

17

<210> 30

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC24199

<400> 30

gcacaagtgg ggtcgg

16

<210> 31

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC24271

<400> 31

ttattgtaat gcaagtgtg

19

<210> 32

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC24272

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<400> 32  
tagctgggag tggaaag 17

<210> 33  
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<220>  
<223> Oligonucleotide ZC24495

<400> 33  
tccaagcgtg accagttcag 20

<210> 34  
<211> 18  
<212> DNA  
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<220>  
<223> Oligonucleotide ZC24496

<400> 34  
agttggcttc tccatccc 18

<210> 35  
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<212> DNA  
<213> Homo sapiens

<400> 35  
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acagataaca ggaaatgata cattccctgt ggtcacttat tctaaaggcc ccaaccttca 120  
aagttcaagt agtgatatgg atgactccac agaaagggag cagtcacgcc ttacttcttg 180  
ccttaagaaa agagaagaaa tgaaactgaa ggagtgtgtt tccatcctcc cacggaagga 240  
aagcccctct gtccgatact ccaaagacgg aaagctgctg gctgcaacct tgctgctggc 300  
actgctgtct tgctgcctca cgggtggtgtc tttctaccag gtggccgccc tgcaagggga 360  
cctggccagc ctccgggcag agctgcaggg ccaccacgcg gagaagctgc cagcaggagc 420  
aggagccccc aaggccggcc tggaggaagc tccagctgtc accgcgggac tgaaaatctt 480  
tgaaccacca gctccaggag aaggcaactc cagtcagaac agcagaaata agcgtgccgt 540  
tcagggtcca gaagaaacag tcaactcaaga ctgcttgcaa ctgattgcag acagtgaaac 600  
accaactata caaaaaggat cttacacatt tgttccatgg cttctcagct ttaaaagggg 660  
aagtgccta gaagaaaaag agaataaaat attggtcaaa gaaactggtt acttttttat 720  
atatggtcag gttttatata ctgataagac ctacgccatg ggacatctaa ttcagaggaa 780

|       |                     |
|-------|---------------------|
| <210> | 36                  |
| <211> | 35                  |
| <212> | DNA                 |
| <213> | Artificial Sequence |

<400> 36  
cgcgcggttt aaacgccacc atggatgact ccaca 35

<210> 37  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide

<400> 37  
gtatacggcg cgcctcacag cagtttcaat gc 32

<210> 38  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide ZC17251

<400> 38  
tctggacgtc ctcctgctgg tatag 25

|       |                     |
|-------|---------------------|
| <210> | 39                  |
| <211> | 25                  |
| <212> | DNA                 |
| <213> | Artificial Sequence |

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| ggcacagcac  | ggggcgatgg | gcgcgtttcg | ggccctgtgc | ggcctggcgc | tgctgtgcgc  | 60  |
| gctcagcctg  | ggtcagcgcc | ccaccggggg | tcccgggtgc | ggccctgggc | gcctcctgct  | 120 |
| tgggacggga  | acggacgcgc | gctgctgccg | ggttcacacg | acgcgctgct | gccgcgatta  | 180 |
| cccgggcgag  | gagtgtgttt | ccgagtggga | ctgcatgtgt | gtccagcctg | aattccactg  | 240 |
| cggagaccct  | tgctgcacga | cctgccggca | ccacccttgt | ccccaggcc  | aggggggtaca | 300 |
| gtcccagggg  | aaattcagtt | ttggcttcca | gtgtatcgac | tgtgcctcgg | ggaccttctc  | 360 |
| cggggggccac | gaaggccact | gcaaaccctg | gacagactgc | accagttcg  | ggtttctcac  | 420 |
| tgtgttccct  | gggaacaaga | cccacaacgc | tgtgtgcgtc | ccagggtccc | cgccggcaga  | 480 |
| gccgcttggg  | tggctgaccg | tcgtcctcct | ggccgtggcc | gcctgcgtcc | tcctcctgac  | 540 |
| ctcggcccag  | cttgactgc  | acatctggca | gctgaggagt | cagtgcattg | ggccccgaga  | 600 |
| gacccagctg  | ctgctggagg | tgccgccgtc | gaccgaagac | gccagaagct | gccagttccc  | 660 |

cgaggaagag cggggcgagc gatcggcaga ggagaagggg cggctgggag acctgtgggt 720  
 gtgagcctgg ctgtcctccg gggccaccga ccgcagccag cccctcccca ggagctcccc 780  
 aggccgcagg gctctgcgtt ctgctctggg ccg 813

<210> 43

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC10.134

<400> 43

atcagcggaa ttcagatctt cagacaaaac tcacacatgc ccac 44

<210> 44

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC10135

<400> 44

ggcagtctct agatcattta cccggagaca gggag 35

<210> 45

<211> 768

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (7)...(759)

<223> Ig Fc sequence

<400> 45

ggatcc atg aag cac ctg tgg ttc ttc ctc ctg ctg gtg gcg gct ccc 48  
 Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro  
 1 5 10

aga tgg gtc ctg tcc gag ccc aga tct tca gac aaa act cac aca tgc 96  
 Arg Trp Val Leu Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys  
 15 20 25 30

00220"9022960

|   |     |
|---|-----|
| cca ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc | 144 |
| Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu |     |
| 35 40 45  |     |
| ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag | 192 |
| Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu |     |
| 50 55 60  |     |
| gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag | 240 |
| Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys |     |
| 65 70 75  |     |
| ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag | 288 |
| Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys |     |
| 80 85 90  |     |
| ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc | 336 |
| Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu |     |
| 95 100 105 110  |     |
| acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag | 384 |
| Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys |     |
| 115 120 125   |     |
| gtc tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa | 432 |
| Val Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys |     |
| 130 135 140   |     |
| gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc | 480 |
| Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser |     |
| 145 150 155   |     |
| cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa | 528 |
| Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys |     |
| 160 165 170   |     |
| ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag | 576 |
| Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln |     |
| 175 180 185 190   |     |
| ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc | 624 |
| Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly |     |
| 195 200 205   |     |

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tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag 672  
 Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln  
                   210                                  215                                  220

cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac 720  
 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn  
                   225                                  230                                  235

cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa taatctaga 768  
 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
                   240                                  245                                  250

<210> 46  
 <211> 52  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide ZC15345

<400> 46  
 ccgtgccag cacctgaagc cgagggggca ccgtcagtct tcctcttccc cc 52

<210> 47  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide ZC15347

<400> 47  
 ggattctaga ttttataccc ggagacaggg a 31

<210> 48  
 <211> 55  
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 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide ZC15517

<400> 48  
 ggtggcggct cccagatggg tcctgtccga gccagatct tcagacaaaa ctcac 55

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<210> 49  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide ZC15530

<400> 49  
 tgggagggct ttgttgga 18

<210> 50  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide ZC15518

<400> 50  
 tccaacaaag ccctcccatc ctccatcgag aaaaccatct cc 42

<210> 51  
 <211> 57  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide ZC15516

<400> 51  
 ggatggatcc atgaagcacc tgtggttctt cctcctgctg gtggcggctc ccagatg 57

<210> 52  
 <211> 59  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide primer

<400> 52  
 ctcagccagg aatccatgc cgagttgaga cgcttccgta gaatgagtgg cctgggccg 59

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<210> 53  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer

<400> 53  
 gcatgtgtga gttttgtctg aagatctggg ctccttcagc cccgggag 48

<210> 54  
 <211> 59  
 <212> DNA  
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<220>  
 <223> Oligonucleotide primer

<400> 54  
 ctcagccagg aaatccatgc cgagttgaga cgcttcgta gaatgagtgg cctgggccc 59

<210> 55  
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 <212> DNA  
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<220>  
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<400> 55  
 gcacggtggg catgtgtgag ttttgtctga agatctgggc tccttcagcc ccgggagag 59

<210> 56  
 <211> 60  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer

<400> 56  
 gcacagaggc tcagaagcaa gtccagctct cccggggctg aaggagccca gatcttcaga 60

<210> 57

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<211> 56  
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<220>  
 <223> Oligonucleotide primer

<400> 57  
 ggggtgggta caacccaga gctgttttaa tctagattat ttacccggag acaggg 56

<210> 58  
 <211> 59  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer

<400> 58  
 ctaacatgtc agcgttattg taatgcaagt gtgaccaatt cagagcccag atcttcaga 59

<210> 59  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Antibody peptide

<400> 59  
 Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Pro Glu Leu Gln Leu Ala  
 1 5 10 15  
 Ile Pro Arg Glu  
 20

<210> 60  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Antibody peptide

<400> 60  
 Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu Asn Lys Glu Leu

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35

1  
Val Lys Glu Thr  
20

5

10

15

09627206 072700